REMARKS

Claims 1-16, 18-60 and 62-112 are pending in the application. Claims 1-8, 15, 16, 18, 30-37, 42-45, 47, 49, 50, 57-60, 62, 63, 75, 77, 79-85 and 89-91 have been rejected. Claims 9-14, 19-28, 38-41, 46, 48, 51-56, 64-71, 73, 76, 78, 86-88, and 92-112 have been withdrawn from consideration. Claims 1-8, 15, 16, 30, 31, 34, 35, 42, 45, 49, 50, 57-60, 62, 63, 75, 77, and 79 have been amended. Support for amendments can be found throughout the specification as originally filed, for example, on pages 21-22, paragraphs 75-78, and in the Examples. Applicants assert that no new matter has been introduced.

Claims 17, 18, 29, 43, 45, 47, 61, 72, 74, and 90 have been canceled without prejudice or disclaimer. In making this cancellation without prejudice, Applicants reserve all rights in these claims to file divisional and/or continuation patent applications.

Remarks to the Oath (Declaration)

In the Office Action, the Examiner alleged that the oath (declaration) is defective because the address of Himangi Jayakar was altered.

Applicants attach hereto a supplemental Declaration. Accordingly Applicants request withdrawal of the objection.

Double Patenting Rejections

In the Office Action, the Examiner provisionally rejected claims 45, 47, 49, 75, 77, 83, 84 and 89-91 under the judicially created doctrine of obviousness-type double patenting as allegedly being unpatentable over claims 1-20 of co-pending Application No. 10/327,673. Applicants disagree. Applicants request the Examiner holds such rejection in abeyance until such time as the Examiner indicates the claims are allowable.

Claim Objections

In the Office Action, the Examiner objected to claims 5, 34, 59 and 81 because of alleged informalities. The Examiner alleged that there is only one nuclear localization signal (NLS) that is to be deleted or mutated in the M protein. Claims 5 and 34 have been amended in order to cure these informalities. Claims 59 and 81 have been cancelled, rendering the objection moot. Accordingly, Applicants request withdrawal of the objection.

CLAIM REJECTIONS

35 U.S.C. § 112 Rejections

Applicants thank the Examiner for noting that the specification is enabling for recombinant VSV M protein with an alanine to methionine substitution at position 33 or 51 or a serine for glycine substitution at position 226 of the protein and for a deletion of amino acids 440-449 in VSV glycoprotein.

The Examiner rejected claims 1-8, 15, 16, 18, 30-37, 43-45, 47, 77, and 79-82 under 35 U.S.C. § 112, first paragraph, as allegedly lacking enablement for claims to a recombinant Rhabdovirus with a mutation within a region encoding the membrane-proximal ectodomain of a Rhabdoviral G protein or mutation in the matrix (M) protein. Applicants disagree.

Applicants submit that one skilled in the art would know how to make and use a recombinant non-cytopathic Rhabdovirus, such as Vesicular Stomatitis Virus (VSV) with a mutation in the matrix (M) protein, as claimed and described in the subject Application. The subject application describes substitution of amino acids 33, 51, 133 and 226, for example in paragraph 222, and deletion of the entire matrix coding sequences and other mutations that results in reduced expression of the matrix sequences (see for example, pages 21-22, paragraphs 75-78). Examples 1-4 and accompanying figures 2, 10 and 11 describe embodied mutations in the M protein resulting in infectious yet non-cytopathic virus. One skilled in the art would necessarily know how to make and use M protein mutated non-cytopathic Rhabdovirus as claimed.

Applicants further submit that one skilled in the art would know how to make and use a recombinant non-cytopathic Rhabdovirus, such as Vesicular Stomatitis Virus (VSV) with a mutation in the glycoprotein (G) protein, as claimed and described in the subject Application. The subject application describes specific amino acid substitutions, for example on pages 24-25, paragraphs 82-86. Examples 5-10 and accompanying figures 21-23, and 28-32 describe embodied mutations in the G protein resulting in infectious yet non-cytopathic virus. One skilled in the art would necessarily know how to make and use G protein-mutated, non-cytopathic Rhabdovirus as claimed. Accordingly, Applicants request withdrawal of the rejection.

35 U.S.C. § 102 Rejections

Applicants thank the Examiner for admitting that claims 1-5, 7, 8, 15-18, 30-34, 36, 37, 43 and 44 are novel in view of Bell *et al.* and claims 1-3, 7, 8, 15, 16, 18, 30, 32, 36, 37, 43 and 44 are novel in view of Conzelmann.

Claims 45, 47, 49, 50, 57, 58, 60, 62, 63, 75, 77, 83-85 and 89-91 are rejected under 35 U.S.C. § 102(e), as allegedly being anticipated by Bell *et al.* (2004/0170607). Applicants disagree. Applicants maintain that the claimed mutations are drawn to a G protein with a mutation in the membrane-proximal ectodomain of the G stem polypeptide, which spans amino acids 421-462 of the G protein (see for example, paragraphs 81-85, pages 23-24, and Examples 5-7 of the specification as originally filed), which results in a Rhabdovirus with decreased viral membrane fusion. The claims are directed to, *inter alia*, specific substitution mutations within this region, *inter alia*, at amino acid positions 457, 461 (SEQ ID NO: 8, 10, 12, 13 and 14), amino acid position 452 (SEQ ID NO: 6), amino acid position 458 (SEQ ID NO: 9) and/or amino acid positions 456 or 457 (SEQ ID NO: 14), and further emphasizes the importance of the region between F440 and N449, which includes the conserved FFGDTG motif, in viral membrane fusion, since deletion of this region completely abolished fusion activity (paragraph 81, page 23). Bell *et al.* describe numerous mutations throughout the VSV genome, but do not specifically describe the claimed substitution or deletion mutations, nor are the methods of use of such recombinant VSV described. Accordingly, Bell *et al.*, do not anticipate claims 45, 47, 49, 50, 57, 58, 60, 62, 63, 75, 77, 83-85 and 89-91. Further, Bell *et al.* do not describe the importance of the G stem nor do they delineate a particular region of the G protein as distinct from any other portion of the G protein in terms of structure or function. Therefore, Bell *et al.* do not describe or provide foundation for the specific mutations of the subject. Accordingly, Applicants request withdrawal of the rejection.

Claims 45, 47, 49, 50, 60, 62, 63, 75, 77, 83-35 and 89-91 are rejected under 35 U.S.C. § 102(b), as being anticipated by Conzelmann (US 6,033,886). Applicants disagree. The instant claims 45, 47, 49, 50, 60, 62, 63, 75, 77, 83-35 and 89-91 are drawn to a Rhabdovirus with a mutation of the **membrane-proximal ectodomain** of the G protein (amino acids 421-462 of the 511-amino acid G-protein), which results in a Rhabdovirus with decreased viral membrane fusion activity. In contrast, Conzelmann describes deletion of the last 46 amino acids of the G protein (i.e. amino acids 465 – 511) (Example 6, column 16, lines 7-8) corresponding to the G protein **cytoplasmic tail** (column 16, lines 18-20), or deletions of the entire G protein (Example 7, column 16), for producing non-infectious rabies virus. The

mutations described in Conzelman do not correspond to the claimed deletions or substitution mutations of the membrane-proximal ectodomain of the G protein, nor does Conzelmann describe the claimed uses of such sequences therefore. Accordingly, Conzelmann does not anticipate claims 45, 47, 49, 50, 60, 62, 63, 75, 77, 83-35 and 89-91. Further, Conzelmann neither describes nor provides a foundation for the importance of any specific portion of the G protein, and certainly not the membrane-proximal ectodomain of the G protein, for inhibiting infection in G protein-mutant rabies viruses. Conzelmann does not delineate a particular region of the G protein as distinct from any other portion of the G protein in terms of structure or function, nor does he describe the specific mutations of the subject application. Accordingly, Applicants request withdrawal of the rejection.

As noted in MPEP Section 821.04, upon indication of allowable claims, claims for process of making and/or using the product which depend from an allowable claim may be rejoined. Accordingly, Applicants request rejoinder of claims 9-14, 19-28, 38-41, 46, 48, 51-56, 64-71, 73, 76, 78, 86-88, and 92-112 upon indication of allowable claims..

In view of the foregoing amendments and remarks, the pending claims are deemed to be allowable. Their favorable reconsideration and allowance is respectfully requested.

Should the Examiner have any question or comment as to the form, content or entry of this Amendment, the Examiner is requested to contact the undersigned at the telephone number below. Similarly, if there are any further issues yet to be resolved to advance the prosecution of this application to issue, the Examiner is requested to telephone the undersigned counsel.

Please charge any fees associated with this paper to deposit account No. 50-3355.

Respectfully submitted,

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Dated: December 13, 2007

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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/656,894	09/08/2003	Michael A. Whitt	P-3558-US	1535

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EXAMINER	
MARVICH, MARIA	
ART UNIT	PAPER NUMBER
1633	
MAIL DATE	DELIVERY MODE
06/14/2007	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/656,894	WHITT ET AL.	
	Examiner	Art Unit	
	Maria B. Marvich, PhD	1633	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *15 March 2007*.

2a)☒ This action is FINAL. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-16,18-60 and 62-112* is/are pending in the application.

4a) Of the above claim(s) *See Continuation Sheet* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-8, 15, 16, 18, 30-37, 42-45, 47, 49, 50, 57-60, 62, 6, 63, 75, 77, 79-85, 89-91* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

Continuation of Disposition of Claims: Claims withdrawn from consideration are 9-14,19-29,38-41,46,48,51-56,64-74,76,78,86-88 and 92-112.

DETAILED ACTION

Any rejection of record in the previous action not addressed in this office action is withdrawn. There are new grounds of rejection herein that were not necessitated by applicants' amendment and therefore, this action is not final.

Information Disclosure Statement

Applicants' statements regarding the documents from the IDS field 5/31/06 that have are acknowledged. More correctly, the statement in the office action mailed 11/14/06 should have stated that the documents were crossed out as they were duplicates.

Oath/Declaration

The oath or declaration is defective. A new oath or declaration in compliance with 37 CFR 1.67(a) identifying this application by application number and filing date is required. See MPEP §§ 602.01 and 602.02.

> The oath or declaration is defective because: Non-initialed and/or non-dated alterations have been made to the oath or declaration. See 37 CFR 1.52(c). Specifically, the address of Himangi Jayakar has been altered.

A copy of a new Declaration has not been received with the response mailed 3/15/07.

Claim Objections

Claims are objected to because of the following informalities: because there is only one nls that is to be deleted or mutated in the M protein, it would be remedial to recite --the nuclear localization sequence-- in claims 5, 34, 59 and 81.

Appropriate correction is required.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 6, 35, 47, 77 and 82 are rejected under are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for a recombinant Rhabdovirus wherein substitution of an alanine amino acid residue for a methionine at position 33 or 51 or serine for a glycine at amino acid position 226 is in the VSV matrix protein and deletion of residues 440-449 is in the glycoprotein of a vesiculovirus does not reasonably provide enablement for any other embodiments. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make or use the invention commensurate in scope with these claims. **This rejection is maintained for reasons of record in the office action mailed 11/3/07 and restated below.**

The test of enablement is whether one skilled in the art could make and use the claimed invention from the disclosures in the patent coupled with information known in the art without undue experimentation (*United States v. Telectronics, Inc.*, 8 USPQ2d 1217 (Fed. Cir. 1988)). Whether undue experimentation is required is not based on a single factor but is rather a conclusion reached by weighing many factors (See *Ex parte Forman*, 230 USPQ 546 (Bd. Pat. App. & Inter, 1986) and In *re Wands*, 8USPQ2d 1400 (Fed. Cir. 1988); these factors include the following:

1) **Nature of invention.** The instant claims are drawn to a recombinant Rhabdovirus (rRV) comprising mutations in sequences encoding the Matrix protein to generate viruses that are non-cytopathic as well as Rhabdovirus comprising mutations in sequences encoding the membrane proximal ectodomain of the Glycoprotein that has reduced infectivity. In other embodiments, the virus has a mutation in the Matrix and Glycoprotein sequences. The vector is used to deliver therapeutic or immunogenic sequences for treatment purposes.

2) **Scope of the invention.** Claims 6, 35, 47, 77 and 82 are drawn to matrix mutations that are substitutions of methionine 33 with alanine and glycoprotein mutations that are deletion of residues 440-449 (elected species). The specification teaches that these recited residues correspond to positions in VSV. No other reference sequence is provided such that no correlative site in other Rhabdoviruses is known.

3) **Number of working examples and guidance.** The specification teaches that previous use of rRV as a vector resulted in cytopathic effects and minimal foreign protein expression due to depressed cellular protein synthesis by Matrix protein function. Applicants specifically propose design of vectors that are non-cytopathic due to mutation of amino acids in Matrix protein. The methods require use of the entire VSV genome in which applicants perform site-directed mutagenesis of VSV to isolate cells with no signs of CPE but expressed reporter protein. The following mutations within M were identified; substitution of amino acid 33, 51, 133 and 226 (see e.g. ¶ 222). Applicants also propose deletion of the entire matrix coding sequences and any other mutation that results in reduced of expression of the matrix sequences (page 22, line 1-70. Applicants identify double mutants that have reduced infectivity due to mutations within the glycoprotein (see e.g. example 4). Applicants teach that the G-stem polypeptide refers to a 42

amino acid membrane proximal ectodomain, a transmembrane anchor domain and a cytoplasmic tail domain of mature G protein. Applicants demonstrate that mutations or insertion of 9-10 amino acids within the membrane proximal ectodomain results in suppressed fusion while deletion of amino acids 440-449 abolished fusion activity and deletion of 449-462 diminished infectivity (see e.g. bridging ¶ page 22-23). Applicants identify mutants E452A, G456D, F458A, W461A, G456DW457A, W457AW461A, W457AF458AW461A and G456DW457DW461A as well as deletion of several domains with the 440-449 and insertion of DAF between 464 and 465 of VSV (see e.g. example 5). .

4) **State of Art**. Rhabdovirus are RNA viruses that comprise six genera including Vesiculoviruses, Lyssavirus and Ephemerovirus obtained from a variety of animal hosts and Novirhabdovirus, cytorhabdovirus and nucleorhabdoviruses are fish, arthropod and plant specific (see Bourhy et al, 2005). At the time of filing (2002), few complete genomic sequences were available and only recently has the available gene-sequence data increased. Current assessment of the taxonomy of the Rhabdoviruses indicates that the major phylogenetic division of the Rhabdoviruses is influenced by mode of transmission and by the host (plant, fish or mammal) and vector (orhtopteran, homopteran or dipteran) species. As well, genetic diversity vary substantially among the genera as demonstrated in figure 3 of Bhoury. Vesicular stomatitis virus infection of eukaryotic cells causes inhibition of nuclear transport which is caused by the matrix (M) protein (see e.g. Petersen, 2001, page 8590, col 2, ¶ 1). This thus results in inhibition of host cell gene expression resulting in cytopathic effects in the host cell leading to apoptosis. The G protein is an N-glycosylated class I-transmembrane protein that forms trimers on the viral

surface to mediate attachment to cellular receptors, endocytosis and fusion with the vesicular membrane.

5) **Unpredictability of the art.** The MPEP teaches, "However, claims reading on significant numbers of inoperative embodiments would render claims non-enabled when the specification does not clearly identify the operative embodiments and undue experimentation is involved in determining those that are operative. Atlas Powder Co. v. E.I. duPont de Nemours & Co., 750 F.2d 1569, 1577, 224 USPQ 409, 414 (Fed. Cir. 1984); In re Cook, 439 F.2d 730, 735, 169 USPQ 298, 302 (CCPA 1971). (see MPEP 2164.08(b).

A review of the art thus demonstrates that the Matrix proteins within the family and even within separate genera are only loosely related. The nucleorhabdoviruses and the Vesiculoviruses share no sequence conservation in the matrix protein (see Luo et al, page 249, col 2, ¶ 2) and even within separate genera; the relationships are not highly conserved. Plant Rhabdoviruses encompass a subgroup of viruses from the Nucleorhabdovirus and the Cytorhabdovirus. Sequence alignment of several of these viruses "have failed to reveal conserved consensus motifs, but short stretches of amino acids display some similarities in composition to the M proteins of other Rhabdoviruses, and the SYNV and RYSV M proteins are more closely related to each other than to other Rhabdovirus proteins" (see Jackson et al, page 642, ¶ 2). Peterson et al provide alignment of 4 highly related Vesiculovirus that demonstrates that inhibition of nuclear transport required a single conserved amino acid which is argued to be due to conserved amino acid correlates to Methionine 51 of VSV (see figure 1). First, this demonstration is limited to only those viruses that are most closely related to VSV. A review of a larger number of Vesiculoviruses show that the relationship amongst the M proteins is not

highly conserved (see Marriot, figure 7) with some Vesiculoviruses sharing 22% homology between Matrix protein sequences (see Taylor et al, page 224, col 2, ¶ 3). Secondly, there is absolutely no conservation in the alignment of Peterson et al at amino acids 33 or amino acid 226. Hence, it is highly unpredictable that assignation of sequences by the designation Met 33 or Met 51 will allow one to identify like sequences amongst highly divergent sequences of such a broad and diverse family of viruses. Similarly, the relationship among the G proteins is too low to allow identification of amino acids 440-449 for any Rhabdovirus. G proteins from different genera share low levels of amino acid sequence identity except for conserved cysteine residues, glycosylation and antigenic domains (see Walker and Kongsuwan, page 1211, col 2, ¶ 1). The plant Rhabdovirus G proteins "have no direct related to G proteins to G proteins of other Rhabdoviruses" (see Jackson et al, page 642, ¶ 2). Walker and Kongsuwan perform a fairly detailed analysis of the structural characteristics of Glycoproteins. Figure 1 is an alignment of 14 species of Rhabdovirus from Vesiculovirus, Lyssavirus, Ephemerovirus and Novirhabdovirus and figure 3 deduced folding models for one from each of these geniuses. The ectodomain is found at the C-terminus of the protein. However, each of the Glycoprotein as well as ectodomains of the proteins have variable length causing confusion as to what actually corresponds to amino acids 440-449. Both the alignment and the models demonstrate that the ability to accurately define the regions that correspond to amino acids 440-449 of the instant specification is highly unpredictable.

6) **Summary**. In view of predictability of the art to which the invention pertains and the lack of guidance in the specification: undue experimentation would be required to practice the claimed methods with reasonable expectation of success, absent a specific and detailed

description in the specification. Given the above analysis of the factors which the courts have determined are critical in determining whether a claimed invention is enabled, it must be concluded that the skilled artisan would have had to have conducted undue unpredictable experimentation in order to practice the claimed invention.

Claims 1-8, 15, 16, 18, 30-37, 43-45, 79-82 are rejected under are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for a deletion or mutation that results in a noncytopathic recombinant Rhabdovirus comprises substitution of an alanine amino acid residue for a methionine at position 33 or 51 or serine for a glycine at amino acid position 226 is in the VSV matrix protein does not reasonably provide enablement for any other embodiments. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make or use the invention commensurate in scope with these claims. **This is a new rejection necessitated by applicants' amendment.**

The claims have been amended to recite that the Rhabdovirus M protein is mutated such that the mutation or deletion results in a non-cytopathic Rhabdovirus. Thus the mutation is responsible for the loss of cytopathicity. The scope of mutations is large as the claims recite that it can be any mutation in the M protein. However, the mutation must result in loss of cytopathicity. Applicants have only disclosed three such mutants, a substitution of alanine to methionine at amino acids 33 or 51 or a serine to glycine substitution at position 226.

Recombinant technology for the generation of fragments is highly developed. However, the ability to determine *a priori* whether a fragment or related sequence can function in the

recited invention is not. As well, a review of the art demonstrates that the ability to *de novo* protein model is not routine but requires vast computation skills (see Protein structure prediction, page 2, first paragraph). This article also teaches that prediction methods that rely on comparative protein modeling allow similar domains or structures to allow identification of three-dimensional models (see Protein structure prediction, page 2, first paragraph). However, as demonstrated by Smith et al, even a single mutation can greatly effect even simple structural formations of the resultant protein. This is explained in the review titled Tertiary structure that teaches mutations in genes encoding proteins can result in degradation or lack of transport or aggregation into insoluble deposits of the resulting protein (begin page 1, last paragraph). Specifically, Tseng and Liang teach that protein surfaces in particular experience very different selective pressure than other functional domains and global protein sequence and structure similarity are often unreliable for function prediction (see Introduction). A particular protein sequence determines the protein's structural, and functional properties, and a predictability of a representative number of claimed polypeptide sequences that display noteworthy biological properties requires a knowledge of and guidance with regard to which amino acids in the protein's sequence, if any, are tolerant of modification and which are conserved (i.e., expectedly intolerant to modification), and detailed knowledge of the ways in which a protein's structure relates to its functional usefulness (see Tertiary structure, Protein structure prediction and Smith et al). , isolation of a protein with one or several amino acids that have been altered by any number of means requires a detailed understanding of the structural requirements of the protein. The specification fails to convey the relevant identifying characteristics of the recited nucleic

acids nor provide a description of the genes such that the structural requirements of the genes are known.

In view of the unpredictability of the art of predicting the functional and structural nature of mutants that lead to loss of cytopathicity: undue experimentation would be required to practice the claimed methods with reasonable expectation of success, absent a specific and detailed description in the specification. Given the unpredictability of the art, the poorly developed state of the art with regard to predicting the structural/ functional characteristics of a protein from primary sequence alone, the lack of adequate working examples and the lack of guidance provided by applicants, the skilled artisan would have to have conducted undue, unpredictable experimentation to practice the claimed invention.

Response to Argument

Applicants traverse the claim rejections under 35 U.S.C. 112, first paragraph on pages 27-28 of the amendment filed 3/15/07. Applicants argue that a person of skill in the art would have been able to identify the important corresponding residues across species even if there was low sequence homology between species. As well, applicants argue that Taylor supports the proposition that it would be routine in the art to align the Rhabdovirus and identify which nucleotides to modify.

Applicants' arguments filed 3/15/07 have been fully considered but they are not persuasive. The instant claims 6, 35, 47, 77 and 82 have been rejected as the claims are drawn to any Rhabdoviral M with a substitution of alanine to methionine at amino acids 33 or 51 or a serine to glycine substitution at position 226 or any Rhabdoviral G protein with a deletion in the

membrane proximal ectodomain from 440 to 449 or 449 to 461. The art of identifying those amino acids in any other Rhabdovirus is highly unpredictable for the following reasons. First, the amino acid sequences do not share significant homology overall or in the recited regions such that those amino acids identified as functional in VSV can be predicted for other Rhabdovirus. While applicants point to Figure 20 of the instant specification, this figure is limited to an alignment of the membrane proximal ectodomain from 7 Rhabdovirus in which all 7 of the viruses are members of the highly conserved species of vesiculovirus. Taylor teaches that Met51 from VSV is conserved with CHPV and SVCV and PIR (all three are vesiculovirus). As well, Asn163 from VSV is conserved in CHPV but not in the other two species. Hence VSV Met51 alone is identifiable in other vesiculovirus according to the published art. However, none of the other recited M protein positions appear to be and the identity of this position in other families is unknown. Secondly, even for Met51, the amino acids positions in other vesiculovirus do not share the same position number in the other vesiculovirus and thus cannot be identified as recited For example, the amino acids corresponding to Met51 and Asn163 in CHPV are Met54 and Asn166.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.
>
> (e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an

international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

Claims 45, 47, 49, 50, 57, 58, 60, 62, 63, 75, 77, 83-85 and 89-91 are rejected under 35 U.S.C. 102(e) as being anticipated by Bell et al (2004/0170607; see entire documents).

Bell et al teach recombinant Rhabdovirus that are mutants of VSV with deletions in the region within the membrane proximal ectodomain that corresponds to 440-449 of the instant specification, as recited in claims 45, 47, 63, 75, 77, 90 and 91. Hence, the Rhabdovirus comprises mutations in the N-terminal portion of the M protein in addition to modifications within the G protein as recited in claims 57 and 58. The G protein is modified (see e.g. ¶ 112) such that the RV expresses for example therapeutic proteins (see e.g. ¶ 113-114) or to encode antireceptors (see e.g. ¶ 112) as recited in claims 49, 50, 84, 85 and 89. The coding sequences is inherently under control of a regulatory element as recited in claims 60 and 83. The Rhabdovirus are vectors designed to act as gene delivery vectors and to deliver antigens as recited in claim 62 and 91 for delivery to cells (see e.g. ¶ 112).

Claims 45, 47, 49, 50, 60, 62, 63, 75, 77, 83-85 and 89-91 are rejected under 35 U.S.C. 102(b) as being anticipated by Conzelmann (US 6,033,886; see entire document).

Conzelmann teaches a recombinant non-cytopathic Rhabdovirus such as VSV (see e.g. col 5, line 39 and col 3-4 bridging ¶) comprising a genome comprising a mutation in the sequence encoding a G protein (G-) (see e.g. col 6, line 29-30) as recited in claims 45, 63, 75 and 90. In the G- Rhabdovirus, the mutation/ deletion in the G sequence can be the entire sequence

and as such encompass a deletion in the 440-449 region (see e.g. col 6, line 36) as recited in claims 47 and 77. The Rhabdovirus inherently comprises a regulatory region for expression of its proteins as recited in claim 60 and 83. The virus comprises heterologous nucleic acids encoding sequences that can be considered therapeutic in that they are used to generate therapies against virulent viruses (see e.g. col 3,line 30-33) as recited in claims 49, 50, 61, 62, 84 and 85 and are additionally inherently associated with regulatory elements for their expression as recited in claims 3, 32, 60 and 83. The heterologous nucleic acids can be epitopes, which often function as anti-receptors as recited in claim 89. Vectors encoding the genomes are taught in col 11, line 10-12 as recited in claim 91.

Response to Argument

Applicants traverse the claim rejections under 35 U.S.C. 102 on pages 28 and 29 of the amendment filed 3/15/07. Applicants' arguments filed 3/15/07 have been fully considered but they are not persuasive for the following reasons. Applicants argue that it was unexpected in light of Bell or Conzelmann et all that mutations of the membrane proximal ectodomain of the G protein that membrane fusion would be inhibited. However, as the claims are drawn to any mutation in the membrane proximal ectodomain of the G protein even those mutants that do not have the intended function anticipate the instant claims.

Double Patenting

A rejection based on double patenting of the "same invention" type finds its support in the language of 35 U.S.C. 101, which states that "whoever invents or discovers any new and useful process ... may obtain a patent therefor ..." (Emphasis added). Thus, the term "same invention," in this context, means an invention drawn to identical subject matter. See *Miller v.*

Eagle Mfg. Co., 151 U.S. 186 (1894); *In re Ockert*, 245 F.2d 467, 114 USPQ 330 (CCPA 1957); and *In re Vogel*, 422 F.2d 438, 164 USPQ 619 (CCPA 1970).

The nonstatutory double patenting rejection is based on a judicially created doctrine grounded in public policy (a policy reflected in the statute) so as to prevent the unjustified or improper timewise extension of the "right to exclude" granted by a patent and to prevent possible harassment by multiple assignees. See *In re Goodman*, 11 F.3d 1046, 29 USPQ2d 2010 (Fed. Cir. 1993); *In re Longi*, 759 F.2d 887, 225 USPQ 645 (Fed. Cir. 1985); *In re Van Ornum*, 686 F.2d 937, 214 USPQ 761 (CCPA 1982); *In re Vogel*, 422 F.2d 438, 164 USPQ 619 (CCPA 1970);and, *In re Thorington*, 418 F.2d 528, 163 USPQ 644 (CCPA 1969).

A timely filed terminal disclaimer in compliance with 37 CFR 1.321(c) may be used to overcome an actual or provisional rejection based on a nonstatutory double patenting ground provided the conflicting application or patent is shown to be commonly owned with this application. See 37 CFR 1.130(b).

Effective January 1, 1994, a registered attorney or agent of record may sign a terminal disclaimer. A terminal disclaimer signed by the assignee must fully comply with 37 CFR 3.73(b).

Claims 45, 47, 49, 75, 77, 83, 84 and 89-91 are provisionally rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claims 1-20 of copending Application No. 10/327,673.

An obviousness-type double patenting rejection is appropriate where the conflicting claims are not identical, but an examined application claim is not patentably distinct from the reference claims because the examined claim is either anticipated by, or would have been obvious over, the reference claims. Although the conflicting claims are not identical, they are not patentably distinct from each other because the cited claims of the instant invention are generic to all that is recited in claims 1-20 of copending Application No. 10/327,673. That is, the cited claims of copending Application No. 10/327,673 anticipate and fall entirely within the scope of the rejected claims of the instant application. Specifically, copending Application No. 10/327,673 claims a recombinant Rhabdovirus comprising a deletion of N-terminal sequences of a VSV G peptide sequence and DNA sequences encoding the Rhabdovirus.

Additionally, if a patent resulting from the instant claims was issued and transferred to an assignee different from the assignee holding the copending Application No. 10/327,673, then two different assignees would hold a patent to the claimed invention of copending Application No. 10/327,673, and thus improperly there would be possible harassment by multiple assignees.

This is a provisional obviousness-type double patenting rejection because the conflicting claims have not in fact been patented.

Response to Argument

It is acknowledged that applicants' will address the provisional obviousness double patenting rejections upon indication of allowable subject matter. However, until the recited claims are patented or a terminal disclaimer is filed, the claims remain rejected.

As well, applicants' arguments filed 3/15/07but are not persuasive as both claims include claims drawn to G proteins with deletions that are generic and not limited to specifically either the membrane proximal ectodomain or deletion of the entire N-terminus. Thus the instant claims by reciting a Rhabdovirus comprising a mutation in a G protein are generic to all that is recited in application 10/327673. However, as the claims are drawn to any mutation in the membrane proximal ectodomain of the G protein even those mutants that do not have the intended function anticipate the instant claims.

Conclusion

Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL.** See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Maria B. Marvich, PhD whose telephone number is (571)-272-0774. The examiner can normally be reached on M-F (7:00-4:00).

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Joseph Woitach, PhD can be reached on (571)-272-0739. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Maria B Marvich, PhD
Examiner
Art Unit 1633

Joe Woitach
AU 1633